

38-21(52806) Sequence Listing_PCT_2.ST25.txt
SEQUENCE LISTING

<110> Monsanto Technology LLC

Baum, James A.
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Engleman, James T.

Krasomil-Osterfeld, Karina

Pitkin, John W.

Roberts, James K.

<120> Insecticidal Proteins Secreted From Bacillus Species and Uses Therefor

<130> 38-21(52806)PCT

<150> US 60/485,483

<151> 2003-07-07

<160> 33

<170> PatentIn version 3.1

<210> 1

<211> 15

<212> PRT

<213> Bacillus thuringiensis

<400> 1

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1 5 10 15

<210> 2

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38-21(52806) Sequence Listing_PCT_2.ST25.txt

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<213> Artificial Sequence

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<213> Bacillus thuringiensis

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<221> CDS

<222> (153)..(1253)

<223>

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aaagcgttat caagagtgat ggagggataa tt atg aaa aat aga ttt tca aaa 173
Met Lys Asn Arg Phe Ser Lys
1 5gtg gca tta tgc acc gta ccg att tta atg gtt tct aca ttc gcc agt 221
Val Ala Leu Cys Thr Val Pro Ile Leu Met Val Ser Thr Phe Ala Ser
10 15 20tca agc atg tca gct ttt gct gca gaa gcc aaa tca cca gat tta aat 269
Ser Ser Met Ser Ala Phe Ala Ala Glu Ala Lys Ser Pro Asp Leu Asn
25 30 35gta tct caa caa gta ata ggt ccc tat gcc gaa tct tat att gat att 317
Val Ser Gln Gln Val Ile Gly Pro Tyr Ala Glu Ser Tyr Ile Asp Ile
40 45 50 55gtg cag gat aga atg aaa caa agg gat aag gga tca aaa tta act ggt 365
Val Gln Asp Arg Met Lys Gln Arg Asp Lys Gly Ser Lys Leu Thr Gly
60 65 70aaa cca ata aat atg caa gaa caa ata ata gat ggg tgg ttt cta gct 413
Lys Pro Ile Asn Met Gln Glu Gln Ile Ile Asp Gly Trp Phe Leu Ala
75 80 85

| 38-21(52806) Sequence Listing_PCT_2.ST25.txt | | | | | | | | | | | | | | | | |
|--|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| aga | ttt | tgg | ata | ttt | aag | gat | caa | aac | aat | aac | cat | cag | aca | aat | aga | |
| Arg | Phe | Trp | Ile | Phe | Lys | Asp | Gln | Asn | Asn | Asn | His | Gln | Thr | Asn | Arg | 461 |
| | | 90 | | | | | 95 | | | | | 100 | | | | |
| ttt | ata | tcc | tgg | ttt | aaa | gat | aat | att | gct | agt | tca | aaa | ggg | tat | aat | 509 |
| Phe | Ile | Ser | Trp | Phe | Lys | Asp | Asn | Ile | Ala | Ser | Ser | Lys | Gly | Tyr | Asn | |
| | 105 | | | | | 110 | | | | | 115 | | | | | |
| agt | att | gcg | gag | caa | atg | ggg | tta | aaa | ata | gaa | gca | gaa | aac | gat | atg | 557 |
| Ser | Ile | Ala | Glu | Gln | Met | Gly | Leu | Lys | Ile | Glu | Ala | Glu | Asn | Asp | Met | |
| 120 | | | | | 125 | | | | | 130 | | | | | 135 | |
| gat | gta | aca | aat | ata | gat | tat | aca | tct | aag | aca | ggc | gat | acc | att | tat | 605 |
| Asp | Val | Thr | Asn | Ile | Asp | Tyr | Thr | Ser | Lys | Thr | Gly | Asp | Thr | Ile | Tyr | |
| | | | | 140 | | | | | 145 | | | | | 150 | | |
| aat | ggg | att | tca | gaa | ttg | aaa | aat | tat | aca | gga | tca | act | caa | aag | atg | 653 |
| Asn | Gly | Ile | Ser | Glu | Leu | Lys | Asn | Tyr | Thr | Gly | Ser | Thr | Gln | Lys | Met | |
| | | | 155 | | | | | 160 | | | | | 165 | | | |
| aaa | aca | gat | agt | ttt | caa | aga | gat | tat | aca | aaa | tca | gaa | tct | act | tca | 701 |
| Lys | Thr | Asp | Ser | Phe | Gln | Arg | Asp | Tyr | Thr | Lys | Ser | Glu | Ser | Thr | Ser | |
| | | 170 | | | | | 175 | | | | | 180 | | | | |
| gta | act | aat | gga | tta | caa | tta | gga | ttt | aaa | gtt | gct | gct | aaa | gga | gta | 749 |
| Val | Thr | Asn | Gly | Leu | Gln | Leu | Gly | Phe | Lys | Val | Ala | Ala | Lys | Gly | Val | |
| | 185 | | | | | 190 | | | | | 195 | | | | | |
| gtt | gct | ttg | gct | ggg | gca | gac | ttt | gaa | acc | agt | gtt | act | tat | aat | cta | 797 |
| Val | Ala | Leu | Ala | Gly | Ala | Asp | Phe | Glu | Thr | Ser | Val | Thr | Tyr | Asn | Leu | |
| 200 | | | | | 205 | | | | | 210 | | | | | 215 | |
| tca | act | act | aca | act | gaa | aca | aat | aca | ata | tca | gac | aag | ttt | act | gtc | 845 |
| Ser | Thr | Thr | Thr | Thr | Glu | Thr | Asn | Thr | Ile | Ser | Asp | Lys | Phe | Thr | Val | |
| | | | | 220 | | | | | 225 | | | | | 230 | | |
| cca | tct | caa | gaa | gtt | aca | ttg | cct | cca | gga | cat | aaa | gcg | ata | gtg | aaa | 893 |
| Pro | Ser | Gln | Glu | Val | Thr | Leu | Pro | Pro | Gly | His | Lys | Ala | Ile | Val | Lys | |
| | | | 235 | | | | | 240 | | | | | 245 | | | |
| cat | gat | tta | aga | aaa | atg | gtt | tat | tct | ggg | act | cat | gat | cta | aag | ggg | 941 |
| His | Asp | Leu | Arg | Lys | Met | Val | Tyr | Ser | Gly | Thr | His | Asp | Leu | Lys | Gly | |
| | | 250 | | | | 255 | | | | | | 260 | | | | |
| gat | tta | att | gtg | agt | ttt | aat | gat | aaa | gag | att | gta | caa | aaa | ttt | att | 989 |
| Asp | Leu | Ile | Val | Ser | Phe | Asn | Asp | Lys | Glu | Ile | Val | Gln | Lys | Phe | Ile | |
| | 265 | | | | | 270 | | | | | 275 | | | | | |
| tat | cca | aat | tat | aga | gaa | att | aat | tta | tct | gat | atc | cgt | gaa | act | atg | 1037 |
| Tyr | Pro | Asn | Tyr | Arg | Glu | Ile | Asn | Leu | Ser | Asp | Ile | Arg | Glu | Thr | Met | |
| 280 | | | | | 285 | | | | | 290 | | | | | 295 | |
| att | gaa | att | gat | gaa | tgg | aat | cat | gta | aac | cct | gtg | aat | ttt | tat | gaa | 1085 |
| Ile | Glu | Ile | Asp | Glu | Trp | Asn | His | Val | Asn | Pro | Val | Asn | Phe | Tyr | Glu | |
| | | | | 300 | | | | | 305 | | | | | 310 | | |
| tta | gtt | ggg | gtc | aaa | aat | cat | ata | aaa | aat | ggg | gaa | act | ttg | tat | ata | 1133 |
| Leu | Val | Gly | Val | Lys | Asn | His | Ile | Lys | Asn | Gly | Glu | Thr | Leu | Tyr | Ile | |
| | | | 315 | | | | | 320 | | | | | 325 | | | |
| gat | act | cca | gct | aaa | ttt | atg | ttt | aat | ggg | gct | aat | cca | tat | tat | aga | 1181 |
| Asp | Thr | Pro | Ala | Lys | Phe | Met | Phe | Asn | Gly | Ala | Asn | Pro | Tyr | Tyr | Arg | |
| | | 330 | | | | | 335 | | | | | 340 | | | | |

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gca aca ttt aca gaa tac gac ggg aat aat aat cct gtt caa aca aag 1229
 Ala Thr Phe Thr Glu Tyr Asp Gly Asn Asn Asn Pro Val Gln Thr Lys
 345 350 355

gta tta agt gaa aac ttt aaa ttg 1253
 Val Leu Ser Glu Asn Phe Lys Leu
 360 365

<210> 4

<211> 367

<212> PRT

<213> Bacillus thuringiensis

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Met Val Ser Thr Phe Ala Ser Ser Ser Met Ser Ala Phe Ala Ala Glu
 20 25 30

Ala Lys Ser Pro Asp Leu Asn Val Ser Gln Gln Val Ile Gly Pro Tyr
 35 40 45

Ala Glu Ser Tyr Ile Asp Ile Val Gln Asp Arg Met Lys Gln Arg Asp
 50 55 60

Lys Gly Ser Lys Leu Thr Gly Lys Pro Ile Asn Met Gln Glu Gln Ile
 65 70 75 80

Ile Asp Gly Trp Phe Leu Ala Arg Phe Trp Ile Phe Lys Asp Gln Asn
 85 90 95

Asn Asn His Gln Thr Asn Arg Phe Ile Ser Trp Phe Lys Asp Asn Ile
 100 105 110

Ala Ser Ser Lys Gly Tyr Asn Ser Ile Ala Glu Gln Met Gly Leu Lys
 115 120 125

Ile Glu Ala Glu Asn Asp Met Asp Val Thr Asn Ile Asp Tyr Thr Ser
 130 135 140

Lys Thr Gly Asp Thr Ile Tyr Asn Gly Ile Ser Glu Leu Lys Asn Tyr
 145 150 155 160

Thr Gly Ser Thr Gln Lys Met Lys Thr Asp Ser Phe Gln Arg Asp Tyr

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 165 170 175

Thr Lys Ser Glu Ser Thr Ser Val Thr Asn Gly Leu Gln Leu Gly Phe
 180 185 190

Lys Val Ala Ala Lys Gly Val Val Ala Leu Ala Gly Ala Asp Phe Glu
 195 200 205

Thr Ser Val Thr Tyr Asn Leu Ser Thr Thr Thr Thr Glu Thr Asn Thr
 210 215 220

Ile Ser Asp Lys Phe Thr Val Pro Ser Gln Glu Val Thr Leu Pro Pro
 225 230 235 240

Gly His Lys Ala Ile Val Lys His Asp Leu Arg Lys Met Val Tyr Ser
 245 250 255

Gly Thr His Asp Leu Lys Gly Asp Leu Ile Val Ser Phe Asn Asp Lys
 260 265 270

Glu Ile Val Gln Lys Phe Ile Tyr Pro Asn Tyr Arg Glu Ile Asn Leu
 275 280 285

Ser Asp Ile Arg Glu Thr Met Ile Glu Ile Asp Glu Trp Asn His Val
 290 295 300

Asn Pro Val Asn Phe Tyr Glu Leu Val Gly Val Lys Asn His Ile Lys
 305 310 315 320

Asn Gly Glu Thr Leu Tyr Ile Asp Thr Pro Ala Lys Phe Met Phe Asn
 325 330 335

Gly Ala Asn Pro Tyr Tyr Arg Ala Thr Phe Thr Glu Tyr Asp Gly Asn
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 355 360 365

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<211> 1621

<212> DNA

<213> Bacillus thuringiensis

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38-21(52806) Sequence Listing_PCT_2.ST25.txt

<221> CDS

<222> (530)..(1621)

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tttatatagg tttcatctaa ttttcaagac atgtgggtgt tttgcgtttt cttcttccaa      180
at ttgataaa tcaagctccc atattcatga atccagcgca taatgattgt gggatgaact      240
gaaacatcac gatagcttaa agcaaaacga caatagtagc ggacggctac cataataata      300
tcttgtttga actgtttccc tttaaaatat cacatttgtg attctcctcg atgctttttt      360
tagagtgtag cttcatctag aacactttgc aatagaacca ttcctttgat atacaattaa      420
accacattta tccttcatgg aatgtttata tattaaagaa tataaaaaaa catacgatgt      480
tataattaat ttgaaagcgt taacaaaaat gaatgatgga gggataatt atg aaa tac      538
                                     Met Lys Tyr
                                     1

aag ttt tca aaa gtc gtt aag tgt act tta cca gct tta atg att act      586
Lys Phe Ser Lys Val Val Lys Cys Thr Leu Pro Ala Leu Met Ile Thr
5                                     10                                     15

aca ttc gtt act cca agt atg gca gtt ttt gcc gca gaa acc aag tcg      634
Thr Phe Val Thr Pro Ser Met Ala Val Phe Ala Ala Glu Thr Lys Ser
20                                     25                                     30                                     35

cca aat cta aat gca tct caa caa gca ata act cca tat gct gaa tct      682
Pro Asn Leu Asn Ala Ser Gln Gln Ala Ile Thr Pro Tyr Ala Glu Ser
40                                     45                                     50

tat att gat act gtt caa gat aga atg aaa caa aga gat agg gaa tca      730
Tyr Ile Asp Thr Val Gln Asp Arg Met Lys Gln Arg Asp Arg Glu Ser
55                                     60                                     65

aaa cta act ggt aaa cca ata aat atg caa gaa caa ata ata gat gga      778
Lys Leu Thr Gly Lys Pro Ile Asn Met Gln Glu Gln Ile Ile Asp Gly
70                                     75                                     80

tgg ttt tta gct aga ttc tgg ata ttt aaa gat caa aat aac aat cat      826
Trp Phe Leu Ala Arg Phe Trp Ile Phe Lys Asp Gln Asn Asn Asn His
85                                     90                                     95

caa aca aat aga ttt ata tcc tgg ttt aaa gat aat ctt gct agt tcg      874
Gln Thr Asn Arg Phe Ile Ser Trp Phe Lys Asp Asn Leu Ala Ser
100                                     105                                     110                                     115

aag ggg tat gac agt ata gca gaa caa atg ggc tta aaa ata gaa gca      922
Lys Gly Tyr Asp Ser Ile Ala Glu Gln Met Gly Leu Lys Ile Glu Ala
120                                     125                                     130

tta aat gat atg gat gta aca aat att gat tat aca tct aaa aca ggt      970
Leu Asn Asp Met Asp Val Thr Asn Ile Asp Tyr Thr Ser Lys Thr Gly

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 135 140 145

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| Asp Thr Ile Tyr Asn Gly Ile Ser Glu Leu Thr Asn Tyr Thr Gly Thr | |
| 150 155 160 | |
| acc caa aaa atg aaa acc gat agt ttt caa aga gat tat aca aaa tct | 1066 |
| Thr Gln Lys Met Lys Thr Asp Ser Phe Gln Arg Asp Tyr Thr Lys Ser | |
| 165 170 175 | |
| gaa tcc act tca gta aca aat ggg tta caa tta gga ttt aaa gtt gct | 1114 |
| Glu Ser Thr Ser Val Thr Asn Gly Leu Gln Leu Gly Phe Lys Val Ala | |
| 180 185 190 195 | |
| gct aag gga gta gtt gca tta gca ggt gca gat ttt gaa aca agt gtt | 1162 |
| Ala Lys Gly Val Val Ala Leu Ala Gly Ala Asp Phe Glu Thr Ser Val | |
| 200 205 210 | |
| acc tat aat tta tca tct act aca act gaa aca aat aca ata tcg gat | 1210 |
| Thr Tyr Asn Leu Ser Ser Thr Thr Glu Thr Asn Thr Ile Ser Asp | |
| 215 220 225 | |
| aag ttt act gtt cca tct caa gaa gtt aca tta tcc cca gga cat aaa | 1258 |
| Lys Phe Thr Val Pro Ser Gln Glu Val Thr Leu Ser Pro Gly His Lys | |
| 230 235 240 | |
| gca gtg gtg aaa cat gat ttg aga aaa atg gtg tat ttt ggg act cat | 1306 |
| Ala Val Val Lys His Asp Leu Arg Lys Met Val Tyr Phe Gly Thr His | |
| 245 250 255 | |
| gat tta aag ggt gat tta aaa gta ggt ttt aat gat aaa gag att gta | 1354 |
| Asp Leu Lys Gly Asp Leu Lys Val Gly Phe Asn Asp Lys Glu Ile Val | |
| 260 265 270 275 | |
| caa aaa ttt att tat cca aat tat aga tca att gat tta tct gat att | 1402 |
| Gln Lys Phe Ile Tyr Pro Asn Tyr Arg Ser Ile Asp Leu Ser Asp Ile | |
| 280 285 290 | |
| cgt aaa aca atg att gaa att gat aaa tgg aat cat gta aat acc att | 1450 |
| Arg Lys Thr Met Ile Glu Ile Asp Lys Trp Asn His Val Asn Thr Ile | |
| 295 300 305 | |
| gac ttt tat caa tta gtt gga gtt aaa aat cat ata aaa aat ggt gat | 1498 |
| Asp Phe Tyr Gln Leu Val Gly Val Lys Asn His Ile Lys Asn Gly Asp | |
| 310 315 320 | |
| act tta tat ata gat acc ccg gcc gaa ttt aca ttt aat gga gct aat | 1546 |
| Thr Leu Tyr Ile Asp Thr Pro Ala Glu Phe Thr Phe Asn Gly Ala Asn | |
| 325 330 335 | |
| cca tat tat aga gca aca ttt aca gaa tac gac gag aac gga aat cct | 1594 |
| Pro Tyr Tyr Arg Ala Thr Phe Thr Glu Tyr Asp Glu Asn Gly Asn Pro | |
| 340 345 350 355 | |
| gtt caa aca aag att tta agt gga aat | 1621 |
| Val Gln Thr Lys Ile Leu Ser Gly Asn | |
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<212> PRT

<213> Bacillus thuringiensis

<400> 6

Met Lys Tyr Lys Phe Ser Lys Val Val Lys Cys Thr Leu Pro Ala Leu
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Thr Lys Ser Pro Asn Leu Asn Ala Ser Gln Gln Ala Ile Thr Pro Tyr
 35 40 45

Ala Glu Ser Tyr Ile Asp Thr Val Gln Asp Arg Met Lys Gln Arg Asp
 50 55 60

Arg Glu Ser Lys Leu Thr Gly Lys Pro Ile Asn Met Gln Glu Gln Ile
 65 70 75 80

Ile Asp Gly Trp Phe Leu Ala Arg Phe Trp Ile Phe Lys Asp Gln Asn
 85 90 95

Asn Asn His Gln Thr Asn Arg Phe Ile Ser Trp Phe Lys Asp Asn Leu
 100 105 110

Ala Ser Ser Lys Gly Tyr Asp Ser Ile Ala Glu Gln Met Gly Leu Lys
 115 120 125

Ile Glu Ala Leu Asn Asp Met Asp Val Thr Asn Ile Asp Tyr Thr Ser
 130 135 140

Lys Thr Gly Asp Thr Ile Tyr Asn Gly Ile Ser Glu Leu Thr Asn Tyr
 145 150 155 160

Thr Gly Thr Thr Gln Lys Met Lys Thr Asp Ser Phe Gln Arg Asp Tyr
 165 170 175

Thr Lys Ser Glu Ser Thr Ser Val Thr Asn Gly Leu Gln Leu Gly Phe
 180 185 190

Lys Val Ala Ala Lys Gly Val Val Ala Leu Ala Gly Ala Asp Phe Glu
 195 200 205

Thr Ser Val Thr Tyr Asn Leu Ser Ser Thr Thr Thr Glu Thr Asn Thr
 210 215 220

38-21(52806) Sequence Listing_PCT_2.ST25.txt

Ile Ser Asp Lys Phe Thr Val Pro Ser Gln Glu Val Thr Leu Ser Pro
 225 230 235 240

Gly His Lys Ala Val Val Lys His Asp Leu Arg Lys Met Val Tyr Phe
 245 250 255

Gly Thr His Asp Leu Lys Gly Asp Leu Lys Val Gly Phe Asn Asp Lys
 260 265 270

Glu Ile Val Gln Lys Phe Ile Tyr Pro Asn Tyr Arg Ser Ile Asp Leu
 275 280 285

Ser Asp Ile Arg Lys Thr Met Ile Glu Ile Asp Lys Trp Asn His Val
 290 295 300

Asn Thr Ile Asp Phe Tyr Gln Leu Val Gly Val Lys Asn His Ile Lys
 305 310 315 320

Asn Gly Asp Thr Leu Tyr Ile Asp Thr Pro Ala Glu Phe Thr Phe Asn
 325 330 335

Gly Ala Asn Pro Tyr Tyr Arg Ala Thr Phe Thr Glu Tyr Asp Glu Asn
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Gly Asn Pro Val Gln Thr Lys Ile Leu Ser Gly Asn
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<213> Bacillus thuringiensis

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 gctagaatat aatgagagc gctaacaaaa aataatggag ggataatc atg aaa tac 177

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Met Lys Tyr
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| aaa tca tca aaa gta gca ata tgt act tta tca gct tta atg ctt tca | 225 |
| Lys Ser Ser Lys Val Ala Ile Cys Thr Leu Ser Ala Leu Met Leu Ser | |
| 5 10 15 | |
| aca att ggt act tcg agt atg tcc act ttt gct gca gaa aca aca tta | 273 |
| Thr Ile Gly Thr Ser Ser Met Ser Thr Phe Ala Glu Thr Thr Leu | |
| 20 25 30 35 | |
| cca ggt caa act ctt aag gaa caa tca ata acc cca cgt gca gaa tct | 321 |
| Pro Gly Gln Thr Leu Lys Glu Gln Ser Ile Thr Pro Arg Ala Glu Ser | |
| 40 45 50 | |
| tat att gat att gta caa gat aga atg aaa caa agg gat ata gaa tcg | 369 |
| Tyr Ile Asp Ile Val Gln Asp Arg Met Lys Gln Arg Asp Ile Glu Ser | |
| 55 60 65 | |
| aaa cgt act ggt aaa ccg att aat atg caa gaa caa ata ata gat gga | 417 |
| Lys Arg Thr Gly Lys Pro Ile Asn Met Gln Glu Gln Ile Ile Asp Gly | |
| 70 75 80 | |
| tgg ttt tta gca aga ttc tgg ata ttt aaa gat caa aat aat aac cat | 465 |
| Trp Phe Leu Ala Arg Phe Trp Ile Phe Lys Asp Gln Asn Asn Asn His | |
| 85 90 95 | |
| caa aca aat aga ttc ata aca tgg ttt aaa aat aat gtt gcc agc tca | 513 |
| Gln Thr Asn Arg Phe Ile Thr Trp Phe Lys Asn Asn Val Ala Ser Ser | |
| 100 105 110 115 | |
| aaa ggt tat gag ggt att gca gaa caa atg ggt ttg aaa ata gaa tcg | 561 |
| Lys Gly Tyr Glu Gly Ile Ala Glu Gln Met Gly Leu Lys Ile Glu Ser | |
| 120 125 130 | |
| atg agt gat atg aat gta tcg aat ata aat tat aca ggt aaa aag ggt | 609 |
| Met Ser Asp Met Asn Val Ser Asn Ile Asn Tyr Thr Gly Lys Lys Gly | |
| 135 140 145 | |
| gat act ata tat aat ggc gtt tcg gaa tta gaa aat aaa atg gga aca | 657 |
| Asp Thr Ile Tyr Asn Gly Val Ser Glu Leu Glu Asn Lys Met Gly Thr | |
| 150 155 160 | |
| cct caa aaa atg aaa tca gat agt ttt caa aga gat tat acc aaa tct | 705 |
| Pro Gln Lys Met Lys Ser Asp Ser Phe Gln Arg Asp Tyr Thr Lys Ser | |
| 165 170 175 | |
| caa tca acc tca gta aca aat ggg tta caa tta gga gtt aaa gtt tct | 753 |
| Gln Ser Thr Ser Val Thr Asn Gly Leu Gln Leu Gly Val Lys Val Ser | |
| 180 185 190 195 | |
| gcc aaa ggt acg gtt gtc tta gga gag gca agc ctt gaa aca agc gtt | 801 |
| Ala Lys Gly Thr Val Val Leu Gly Glu Ala Ser Leu Glu Thr Ser Val | |
| 200 205 210 | |
| act tat aat tta tcg tct act gca act gaa aca gat aca aca tcg gac | 849 |
| Thr Tyr Asn Leu Ser Ser Thr Ala Thr Glu Thr Asp Thr Thr Ser Asp | |
| 215 220 225 | |
| aag ttt act gtc cca tcc caa gaa gtt aca tta cca cca gga cat aaa | 897 |
| Lys Phe Thr Val Pro Ser Gln Glu Val Thr Leu Pro Pro Gly His Lys | |
| 230 235 240 | |

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| | |
|---|------|
| gca gta att aag cat gat tta aga aaa atg gtg tat tct ggt acg cat Ala Val Ile Lys His Asp Leu Arg Lys Met Val Tyr Ser Gly Thr His 245 250 255 | 945 |
| gac tta aag ggg gat tta aaa gta gct ttt aac gat aaa gca att gta Asp Leu Lys Gly Asp Leu Lys Val Ala Phe Asn Asp Lys Ala Ile Val 260 265 270 275 | 993 |
| caa aaa ttt att tat cca aat tat aga tct ata aat tta tct gat att Gln Lys Phe Ile Tyr Pro Asn Tyr Arg Ser Ile Asn Leu Ser Asp Ile 280 285 290 | 1041 |
| cgt aaa aca atg aaa gaa att gat gaa tgg aat cat gta aaa ccc att Arg Lys Thr Met Lys Glu Ile Asp Glu Trp Asn His Val Lys Pro Ile 295 300 305 | 1089 |
| gat ttt tat caa ctg gtt gga ata aaa aat cat ata aaa aat ggg gat Asp Phe Tyr Gln Leu Val Gly Ile Lys Asn His Ile Lys Asn Gly Asp 310 315 320 | 1137 |
| acc tta tat ata gag act cca gct aaa ttt att ttt aat gga gct aat Thr Leu Tyr Ile Glu Thr Pro Ala Lys Phe Ile Phe Asn Gly Ala Asn 325 330 335 | 1185 |
| gta tat tat aga gca act ttt aca gaa tat gat aag gat gga aaa cct Val Tyr Tyr Arg Ala Thr Phe Thr Glu Tyr Asp Lys Asp Gly Lys Pro 340 345 350 355 | 1233 |
| gtt caa ttc aac aaa ttt tta agt gaa aat tac aag tta tagaggaagt Val Gln Phe Asn Lys Phe Leu Ser Glu Asn Tyr Lys Leu 360 365 | 1282 |
| aaagatgccg tagtgagatc gtttcacagc tactgagtat tcaaataata cacgggaaaa | 1342 |
| ttcaccttcc tggaaggacg gatttacttt ttttacggag gaacttgttt tatacatcaa | 1402 |
| aatgtttttt tatgaggttt gtgtattcct atttgagcct ggaacggaac cattttgagt | 1462 |
| aagcttaatt tgacttgga atgtattttt attaccttat tacgtgaaca atggcctata | 1522 |
| aacgtgccac acaggaatgg gaggacgagt | 1552 |

<210> 8

<211> 368

<212> PRT

<213> Bacillus thuringiensis

<400> 8

Met Lys Tyr Lys Ser Ser Lys Val Ala Ile Cys Thr Leu Ser Ala Leu
1 5 10 15

Met Leu Ser Thr Ile Gly Thr Ser Ser Met Ser Thr Phe Ala Ala Glu
20 25 30

38-21(52806) Sequence Listing_PCT_2.ST25.txt

Thr Thr Leu Pro Gly Gln Thr Leu Lys Glu Gln Ser Ile Thr Pro Arg
 35 40 45
 Ala Glu Ser Tyr Ile Asp Ile Val Gln Asp Arg Met Lys Gln Arg Asp
 50 55 60
 Ile Glu Ser Lys Arg Thr Gly Lys Pro Ile Asn Met Gln Glu Gln Ile
 65 70 75 80
 Ile Asp Gly Trp Phe Leu Ala Arg Phe Trp Ile Phe Lys Asp Gln Asn
 85 90 95
 Asn Asn His Gln Thr Asn Arg Phe Ile Thr Trp Phe Lys Asn Asn Val
 100 105 110
 Ala Ser Ser Lys Gly Tyr Glu Gly Ile Ala Glu Gln Met Gly Leu Lys
 115 120 125
 Ile Glu Ser Met Ser Asp Met Asn Val Ser Asn Ile Asn Tyr Thr Gly
 130 135 140
 Lys Lys Gly Asp Thr Ile Tyr Asn Gly Val Ser Glu Leu Glu Asn Lys
 145 150 155 160
 Met Gly Thr Pro Gln Lys Met Lys Ser Asp Ser Phe Gln Arg Asp Tyr
 165 170 175
 Thr Lys Ser Gln Ser Thr Ser Val Thr Asn Gly Leu Gln Leu Gly Val
 180 185 190
 Lys Val Ser Ala Lys Gly Thr Val Val Leu Gly Glu Ala Ser Leu Glu
 195 200 205
 Thr Ser Val Thr Tyr Asn Leu Ser Ser Thr Ala Thr Glu Thr Asp Thr
 210 215 220
 Thr Ser Asp Lys Phe Thr Val Pro Ser Gln Glu Val Thr Leu Pro Pro
 225 230 235 240
 Gly His Lys Ala Val Ile Lys His Asp Leu Arg Lys Met Val Tyr Ser
 245 250 255
 Gly Thr His Asp Leu Lys Gly Asp Leu Lys Val Ala Phe Asn Asp Lys
 260 265 270
 Ala Ile Val Gln Lys Phe Ile Tyr Pro Asn Tyr Arg Ser Ile Asn Leu
 275 280 285

38-21(52806) Sequence Listing_PCT_2.ST25.txt

Ser Asp Ile Arg Lys Thr Met Lys Glu Ile Asp Glu Trp Asn His Val
 290 295 300

Lys Pro Ile Asp Phe Tyr Gln Leu Val Gly Ile Lys Asn His Ile Lys
 305 310 315 320

Asn Gly Asp Thr Leu Tyr Ile Glu Thr Pro Ala Lys Phe Ile Phe Asn
 325 330 335

Gly Ala Asn Val Tyr Tyr Arg Ala Thr Phe Thr Glu Tyr Asp Lys Asp
 340 345 350

Gly Lys Pro Val Gln Phe Asn Lys Phe Leu Ser Glu Asn Tyr Lys Leu
 355 360 365

<210> 9

<211> 1378

<212> DNA

<213> Bacillus thuringiensis

<220>

<221> CDS

<222> (215)..(1306)

<223>

<400> 9
 cagtggatag gaatttgttt tcgtgctagg tatcaattta atttgttcta taagataagt 60
 gaagtacgat caaaatgaat acttttgtgt attagatcaa taggtaaaat aataataaat 120
 tttatatattg aaccttaaaa aattatttaa tcaaattcttt ttcactttaa aaacaaaata 180
 tccagaaaaa acaatagtta acggagggat aata atg aaa tac aag tca tca aaa 235
 Met Lys Tyr Lys Ser Ser Lys
 1 5
 gta gca atg tgt aca tta tca gct tta atg ctt tcg aca atc gcc act 283
 Val Ala Met Cys Thr Leu Ser Ala Leu Met Leu Ser Thr Ile Ala Thr
 10 15 20
 cca agt ata tct gtt ttc gct gca gaa aca act tcg tca cat gcg gtt 331
 Pro Ser Ile Ser Val Phe Ala Ala Glu Thr Thr Ser Ser His Ala Val
 25 30 35
 act aat cag caa aca att acg cag cgt gca gaa tct tat att gat att 379
 Thr Asn Gln Gln Thr Ile Thr Gln Arg Ala Glu Ser Tyr Ile Asp Ile
 40 45 50 55

38-21(52806) Sequence Listing_PCT_2.ST25.txt

| | |
|---|------|
| gtg cac aat aga atg aaa caa aga gat att gaa tca aaa atg aca ggt Val His Asn Arg Met Lys Gln Arg Asp Ile Glu Ser Lys Met Thr Gly 60 65 70 | 427 |
| aaa tcc att aat atg caa gaa caa ata att gat gga tgg ttt tta gct Lys Ser Ile Asn Met Gln Glu Gln Ile Ile Asp Gly Trp Phe Leu Ala 75 80 85 | 475 |
| aga ttt tgg ata ttt aag gat caa aat aat agt cac caa aca aat aga Arg Phe Trp Ile Phe Lys Asp Gln Asn Asn Ser His Gln Thr Asn Arg 90 95 100 | 523 |
| ttt att tca tgg ttt aag gat aat ttg gct agc cca gga ggg tat gat Phe Ile Ser Trp Phe Lys Asp Asn Leu Ala Ser Pro Gly Gly Tyr Asp 105 110 115 | 571 |
| agt atc gct gaa cag atg ggc cta aaa gta gca gca tta aat gat atg Ser Ile Ala Glu Gln Met Gly Leu Lys Val Ala Ala Leu Asn Asp Met 120 125 130 135 | 619 |
| gat ata tca aat gta aat tat act tct aag aca ggg gat act ata tat Asp Ile Ser Asn Val Asn Tyr Thr Ser Lys Thr Gly Asp Thr Ile Tyr 140 145 150 | 667 |
| aat ggt gtt tca gaa tta aaa aat atc aca gga aca act caa aaa atg Asn Gly Val Ser Glu Leu Lys Asn Ile Thr Gly Thr Thr Gln Lys Met 155 160 165 | 715 |
| aaa aca gat agt ttt caa aga gat tat aca aaa tcc cag tca act tca Lys Thr Asp Ser Phe Gln Arg Asp Tyr Thr Lys Ser Gln Ser Thr Ser 170 175 180 | 763 |
| atc acc aat gga tta caa tta gga ttt aaa gtt tca gct aaa gga ata Ile Thr Asn Gly Leu Gln Leu Gly Phe Lys Val Ser Ala Lys Gly Ile 185 190 195 | 811 |
| gtg gcc tta gcc ggt gcg gat ttt gaa gca agt gta aac tat aat tta Val Ala Leu Ala Gly Ala Asp Phe Glu Ala Ser Val Asn Tyr Asn Leu 200 205 210 215 | 859 |
| tcc act acc gca act gaa acc aat aca ata tct gat aaa ttt acc gtt Ser Thr Thr Ala Thr Glu Thr Asn Thr Ile Ser Asp Lys Phe Thr Val 220 225 230 | 907 |
| cct tca caa gaa gtc aca tta gcg cca gga cat aag gcg atc gta aaa Pro Ser Gln Glu Val Thr Leu Ala Pro Gly His Lys Ala Ile Val Lys 235 240 245 | 955 |
| cat agt ttg aag aaa atg gta tac tct gga acg cat gat tta aaa gga His Ser Leu Lys Lys Met Val Tyr Ser Gly Thr His Asp Leu Lys Gly 250 255 260 | 1003 |
| gat tta aca att act ttt aat gat aag gat tta gtt caa aaa ttt att Asp Leu Thr Ile Thr Phe Asn Asp Lys Asp Leu Val Gln Lys Phe Ile 265 270 275 | 1051 |
| tat cca aat tat aaa gct att gat tta tct aat att cgt aaa gca atg Tyr Pro Asn Tyr Lys Ala Ile Asp Leu Ser Asn Ile Arg Lys Ala Met 280 285 290 295 | 1099 |
| aca gaa att gat gaa tgg aat cat gta aaa cct acc gat ttc tat caa Thr Glu Ile Asp Glu Trp Asn His Val Lys Pro Thr Asp Phe Tyr Gln 1147 | |

38-21(52806) Sequence Listing_PCT_2.ST25.txt
 300 305 310

tta gtt ggg aat aaa aat tat ata aaa aac ggg gac act tta tac atc 1195
 Leu Val Gly Asn Lys Asn Tyr Ile Lys Asn Gly Asp Thr Leu Tyr Ile
 315 320 325

gaa aca cct gct aaa ttc act ttg aat gga ggc aac cct tat tat aca 1243
 Glu Thr Pro Ala Lys Phe Thr Leu Asn Gly Gly Asn Pro Tyr Tyr Thr
 330 335 340

gca acc ttt acg gaa tat gat gaa aat gga aat caa gtc aaa aca aag 1291
 Ala Thr Phe Thr Glu Tyr Asp Glu Asn Gly Asn Gln Val Lys Thr Lys
 345 350 355

cgt tta aat aac aaa taagttactt aaaggtaatt cattaacaat gtatccatta 1346
 Arg Leu Asn Asn Lys
 360

tataattaat ttataaaaat aatgttttaa aa 1378

<210> 10

<211> 364

<212> PRT

<213> Bacillus thuringiensis

<400> 10

Met Lys Tyr Lys Ser Ser Lys Val Ala Met Cys Thr Leu Ser Ala Leu
 1 5 10 15

Met Leu Ser Thr Ile Ala Thr Pro Ser Ile Ser Val Phe Ala Ala Glu
 20 25 30

Thr Thr Ser Ser His Ala Val Thr Asn Gln Gln Thr Ile Thr Gln Arg
 35 40 45

Ala Glu Ser Tyr Ile Asp Ile Val His Asn Arg Met Lys Gln Arg Asp
 50 55 60

Ile Glu Ser Lys Met Thr Gly Lys Ser Ile Asn Met Gln Glu Gln Ile
 65 70 75 80

Ile Asp Gly Trp Phe Leu Ala Arg Phe Trp Ile Phe Lys Asp Gln Asn
 85 90 95

Asn Ser His Gln Thr Asn Arg Phe Ile Ser Trp Phe Lys Asp Asn Leu
 100 105 110

Ala Ser Pro Gly Gly Tyr Asp Ser Ile Ala Glu Gln Met Gly Leu Lys
 115 120 125

38-21(52806) Sequence Listing_PCT_2.ST25.txt

Val Ala Ala Leu Asn Asp Met Asp Ile Ser Asn Val Asn Tyr Thr Ser
 130 135 140
 Lys Thr Gly Asp Thr Ile Tyr Asn Gly Val Ser Glu Leu Lys Asn Ile
 145 150 155 160
 Thr Gly Thr Thr Gln Lys Met Lys Thr Asp Ser Phe Gln Arg Asp Tyr
 165 170 175
 Thr Lys Ser Gln Ser Thr Ser Ile Thr Asn Gly Leu Gln Leu Gly Phe
 180 185 190
 Lys Val Ser Ala Lys Gly Ile Val Ala Leu Ala Gly Ala Asp Phe Glu
 195 200 205
 Ala Ser Val Asn Tyr Asn Leu Ser Thr Thr Ala Thr Glu Thr Asn Thr
 210 215 220
 Ile Ser Asp Lys Phe Thr Val Pro Ser Gln Glu Val Thr Leu Ala Pro
 225 230 235 240
 Gly His Lys Ala Ile Val Lys His Ser Leu Lys Lys Met Val Tyr Ser
 245 250 255
 Gly Thr His Asp Leu Lys Gly Asp Leu Thr Ile Thr Phe Asn Asp Lys
 260 265 270
 Asp Leu Val Gln Lys Phe Ile Tyr Pro Asn Tyr Lys Ala Ile Asp Leu
 275 280 285
 Ser Asn Ile Arg Lys Ala Met Thr Glu Ile Asp Glu Trp Asn His Val
 290 295 300
 Lys Pro Thr Asp Phe Tyr Gln Leu Val Gly Asn Lys Asn Tyr Ile Lys
 305 310 315 320
 Asn Gly Asp Thr Leu Tyr Ile Glu Thr Pro Ala Lys Phe Thr Leu Asn
 325 330 335
 Gly Gly Asn Pro Tyr Tyr Thr Ala Thr Phe Thr Glu Tyr Asp Glu Asn
 340 345 350
 Gly Asn Gln Val Lys Thr Lys Arg Leu Asn Asn Lys
 355 360

<210> 11.

38-21(52806) Sequence Listing_PCT_2.ST25.txt

<211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> probe sequence, or amplification primer sequence for use with primer as set forth in SEQ ID NO 12, corresponding to CDS as set forth in SEQ ID NO 3 from 438-458, biased toward codons preferred in Bacillus species genes containing A or T in 3rd position

 <400> 11
 aataataatc atcaaacwaa t 21

 <210> 12
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> probe sequence, or amplification primer sequence for use with SEQ ID NO 11 corresponding to SEQ ID NO 3 from nucleotide position 978- 998, biased toward codons preferred in Bacillus species genes in which A or T is in 3rd position

 <400> 12
 attwggataw ataaattttt g 21

 <210> 13
 <211> 1101
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> coding sequence preferred for use in monocot species encoding a B t TIC901 amino acid sequence variant

 <220>
 <221> CDS
 <222> (1)..(1101)
 <223>

38-21(52806) Sequence Listing_PCT_2.ST25.txt

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<400> 13
atg aag aac cgc ttc agc aag gtc gcc ctc tgc acg gtg cct atc ctc      48
Met Lys Asn Arg Phe Ser Lys Val Ala Leu Cys Thr Val Pro Ile Leu
1 5 10 15

atg gtt tct acg ttc gcg tcc agc tcg atg tcc gcg ttc gca gcg gag      96
Met Val Ser Thr Phe Ala Ser Ser Ser Met Ser Ala Phe Ala Ala Glu
20 25 30

gcc aaa agt cct gac ttg aac gtg tcc caa cag gtc ata ggc cct tac      144
Ala Lys Ser Pro Asp Leu Asn Val Ser Gln Gln Val Ile Gly Pro Tyr
35 40 45

gca gaa tct tac atc gac atc gtc cag gac aga atg aag cag aga gac      192
Ala Glu Ser Tyr Ile Asp Ile Val Gln Asp Arg Met Lys Gln Arg Asp
50 55 60

aaa gga tcc aaa ctc act ggc aaa ccc atc aac atg caa gag cag atc      240
Lys Gly Ser Lys Leu Thr Gly Lys Pro Ile Asn Met Gln Glu Gln Ile
65 70 75 80

atc gat ggg tgg ttt ctc gca cga ttc tgg att ttc aag gat cag aac      288
Ile Asp Gly Trp Phe Leu Ala Arg Phe Trp Ile Phe Lys Asp Gln Asn
85 90 95

aat aac cac cag aca aac agg ttc atc tca tgg ttt aag gat aac atc      336
Asn Asn His Gln Thr Asn Arg Phe Ile Ser Trp Phe Lys Asp Asn Ile
100 105 110

gcc tca tct aag gga tac aac tca ata gcc gaa cag atg ggc ctc aaa      384
Ala Ser Ser Lys Gly Tyr Asn Ser Ile Ala Glu Gln Met Gly Leu Lys
115 120 125

atc gaa gca gag aat gat atg gac gtg aca aat atc gac tac act agt      432
Ile Glu Ala Glu Asn Asp Met Asp Val Thr Asn Ile Asp Tyr Thr Ser
130 135 140

aag acc gga gac aca atc tac aac ggc att tcg gaa ctt aaa aac tat      480
Lys Thr Gly Asp Thr Ile Tyr Asn Gly Ile Ser Glu Leu Lys Asn Tyr
145 150 155 160

acg ggc agc acc cag aaa atg aag acc gat agc ttt caa agg gac tac      528
Thr Gly Ser Thr Gln Lys Met Lys Thr Asp Ser Phe Gln Arg Asp Tyr
165 170 175

aca aaa tcc gag tcg acc tcc gtg acc aat ggc ctc cag ctg ggc ttc      576
Thr Lys Ser Glu Ser Thr Ser Val Thr Asn Gly Leu Gln Leu Gly Phe
180 185 190

aag gtg gca gca aag ggc gtc gtc gct tta gcc ggc gca gac ttc gag      624
Lys Val Ala Ala Lys Gly Val Val Ala Leu Ala Gly Ala Asp Phe Glu
195 200 205

act tcg gtg acc tac aat ctg tct aca act acg act gag acg aac aca      672
Thr Ser Val Thr Tyr Asn Leu Ser Thr Thr Thr Thr Glu Thr Asn Thr
210 215 220

att tcc gac aag ttt acg gtt ccg tct cag gag gtt acg ttc cct cca      720
Ile Ser Asp Lys Phe Thr Val Pro Ser Gln Glu Val Thr Phe Pro Pro
225 230 235 240

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38-21(52806) sequence Listing_PCT_2.ST25.txt

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ggc cac aag gca atc gtc aag cac gac ctg agg aaa atg gtc tac agc      768
Gly His Lys Ala Ile Val Lys His Asp Leu Arg Lys Met Val Tyr Ser
                245                250                255

ggc acc cat gat ctc aaa ggc gac ctc atc gtg tcg ttc aac gac aag      816
Gly Thr His Asp Leu Lys Gly Asp Leu Ile Val Ser Phe Asn Asp Lys
                260                265                270

gag ata gtc cag aag ttc atc tac cca aat tac cgc gac atc aac ctc      864
Glu Ile Val Gln Lys Phe Ile Tyr Pro Asn Tyr Arg Asp Ile Asn Leu
                275                280                285

agt gac atc cga gag acc atg atc gag atc gac gag tgg aac cac gtg      912
Ser Asp Ile Arg Glu Thr Met Ile Glu Ile Asp Glu Trp Asn His Val
                290                295                300

aac cct gtc aat ttc tac gaa ctc gta gga gtt aag aac cac atc aag      960
Asn Pro Val Asn Phe Tyr Glu Leu Val Gly Val Lys Asn His Ile Lys
                305                310                315                320

aac ggt gaa aca ttg tac atc gac acg ccg gct aag ttc atg ttc aac     1008
Asn Gly Glu Thr Leu Tyr Ile Asp Thr Pro Ala Lys Phe Met Phe Asn
                325                330                335

gga gcg aat cct tac tat cga gct acc ttc acg gag tac gat ggc aac     1056
Gly Ala Asn Pro Tyr Tyr Arg Ala Thr Phe Thr Glu Tyr Asp Gly Asn
                340                345                350

aac aat cct gtt cag acc aag gtg ttg agt gag aat ttc aag ctg      1101
Asn Asn Pro Val Gln Thr Lys Val Leu Ser Glu Asn Phe Lys Leu
                355                360                365

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<210> 14

<211> 367

<212> PRT

<213> Artificial Sequence

<220>

<223> coding sequence preferred for use in monocot species encoding a B
t TIC901 amino acid sequence variant

<400> 14

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Met Lys Asn Arg Phe Ser Lys Val Ala Leu Cys Thr Val Pro Ile Leu
1          5          10          15

```

```

Met Val Ser Thr Phe Ala Ser Ser Ser Met Ser Ala Phe Ala Ala Glu
                20          25          30

```

```

Ala Lys Ser Pro Asp Leu Asn Val Ser Gln Gln Val Ile Gly Pro Tyr
35          40          45

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38-21(52806) Sequence Listing_PCT_2.ST25.txt

Ala Glu Ser Tyr Ile Asp Ile Val Gln Asp Arg Met Lys Gln Arg Asp
 50 55 60

Lys Gly Ser Lys Leu Thr Gly Lys Pro Ile Asn Met Gln Glu Gln Ile
 65 70 75 80

Ile Asp Gly Trp Phe Leu Ala Arg Phe Trp Ile Phe Lys Asp Gln Asn
 85 90 95

Asn Asn His Gln Thr Asn Arg Phe Ile Ser Trp Phe Lys Asp Asn Ile
 100 105 110

Ala Ser Ser Lys Gly Tyr Asn Ser Ile Ala Glu Gln Met Gly Leu Lys
 115 120 125

Ile Glu Ala Glu Asn Asp Met Asp Val Thr Asn Ile Asp Tyr Thr Ser
 130 135 140

Lys Thr Gly Asp Thr Ile Tyr Asn Gly Ile Ser Glu Leu Lys Asn Tyr
 145 150 155 160

Thr Gly Ser Thr Gln Lys Met Lys Thr Asp Ser Phe Gln Arg Asp Tyr
 165 170 175

Thr Lys Ser Glu Ser Thr Ser Val Thr Asn Gly Leu Gln Leu Gly Phe
 180 185 190

Lys Val Ala Ala Lys Gly Val Val Ala Leu Ala Gly Ala Asp Phe Glu
 195 200 205

Thr Ser Val Thr Tyr Asn Leu Ser Thr Thr Thr Thr Glu Thr Asn Thr
 210 215 220

Ile Ser Asp Lys Phe Thr Val Pro Ser Gln Glu Val Thr Phe Pro Pro
 225 230 235 240

Gly His Lys Ala Ile Val Lys His Asp Leu Arg Lys Met Val Tyr Ser
 245 250 255

Gly Thr His Asp Leu Lys Gly Asp Leu Ile Val Ser Phe Asn Asp Lys
 260 265 270

Glu Ile Val Gln Lys Phe Ile Tyr Pro Asn Tyr Arg Asp Ile Asn Leu
 275 280 285

Ser Asp Ile Arg Glu Thr Met Ile Glu Ile Asp Glu Trp Asn His Val
 290 295 300

38-21(52806) Sequence Listing_PCT_2.ST25.txt

Asn Pro Val Asn Phe Tyr Glu Leu Val Gly Val Lys Asn His Ile Lys
 305 310 315 320

Asn Gly Glu Thr Leu Tyr Ile Asp Thr Pro Ala Lys Phe Met Phe Asn
 325 330 335

Gly Ala Asn Pro Tyr Tyr Arg Ala Thr Phe Thr Glu Tyr Asp Gly Asn
 340 345 350

Asn Asn Pro Val Gln Thr Lys Val Leu Ser Glu Asn Phe Lys Leu
 355 360 365

<210> 15

<211> 23

<212> DNA

<213> Artificial sequence

<220>

<223> oligonucleotide primer coupled with prJPW152 SEQ ID NO 16 in thermal amplification reactions

<400> 15

cctttggcag aaactttaac tcc

23

<210> 16

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer coupled with prJPW151 SEQ ID NO 15 in thermal amplification reactions

<400> 16

gtgtattctg gtacgcatga c

21

<210> 17

<211> 34

<212> DNA

<213> Artificial Sequence

38-21(52806) Sequence Listing_PCT_2.ST25.txt

<220>

<223> oligonucleotide primer coupled with prJPW183 SEQ ID NO 18 in thermal amplification reactions

<400> 17

gccgatccc tagctgaata tgcagtagat aatg

34

<210> 18

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer coupled with prJPW186 SEQ ID NO 17 in thermal amplification reactions

<400> 18

gtggcacgtt tataggccat tgttc

25

<210> 19

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer coupled with prJPW156 SEQ ID NO 20 in thermal amplification reactions

<400> 19

cttttaggcc catctgttca gcg

23

<210> 20

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer coupled with prJPW155 SEQ ID NO 19 in thermal amplification reactions

38-21(52806) Sequence Listing_PCT_2.ST25.txt

<400> 20
gccttagccg gtgcggattt tgaagc 26

<210> 21

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer coupled with prJPW170 SEQ ID NO 22 in thermal amplification reactions

<400> 21
ggagcttatt tggtatttaa acgctttggt ttgacttgat ttcc 44

<210> 22

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide primer coupled with prJPW168 SEQ ID NO 21 in thermal amplification reactions

<400> 22
gccggatccc agtggatagg aatttgtttt cgtgctagg 39

<210> 23

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> universal forward amplification primer similar to SEQ ID NO:24 and SEQ ID NO:25 that, when used in a thermal amplification reaction with any of SEQ ID NO:27-29 and template DNA homologous to tic901, 1201, 407, 417, or 431 and the like result in amplification of from about 600 to about 650 base pairs

<400> 23
aayatgcarg arcarathat hgaygg 26

38-21(52806) Sequence Listing_PCT_2.ST25.txt

<210> 24
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> universal forward amplification primer similar to SEQ ID NO:23 and SEQ ID NO:25 that, when used in a thermal amplification reaction with any of SEQ ID NO:27-29 and template DNA homologous to tic901, 1201, 407, 417, or 431 and the like result in amplicon of from about 600 to about 650 base pairs

<400> 24
 aayatgcarg arcarathat hga 23

<210> 25
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> universal forward amplification primer similar to SEQ ID NO:23 and SEQ ID NO:24 that, when used in a thermal amplification reaction with any of SEQ ID NO:27-29 and template DNA homologous to tic901, 1201, 407, 417, or 431 and the like result in amplicon of from about 600 to about 650 base pairs

<400> 25
 aayatgcarg arcarathat 20

<210> 26
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> universal forward amplification primer that, when used in a thermal amplification reaction with any of SEQ ID NO:27-29 and template DNA homologous to tic901, 1201, 407, 417, 431 and the like result in amplicon of from about 395 to about 425 base pairs

38-21(52806) Sequence Listing_PCT_2.ST25.txt

<220>

<221> misc_feature

<222> (3)..(3)

<223> inosine

<220>

<221> misc_feature

<222> (9)..(9)

<223> inosine

<400> 26

ggngayacna thtayaaygg

20

<210> 27

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> universal reverse amplification primer similar to SEQ ID NO:28 and SEQ ID NO:29

<220>

<221> misc_feature

<222> (6)..(6)

<223> inosine

<220>

<221> misc_feature

<222> (24)..(24)

<223> inosine

<400> 27

tarttnggrt adatraaytt ytnac

26

38-21(52806) Sequence Listing_PCT_2.ST25.txt

<210> 28
<211> 23
<212> DNA
<213> Artificial sequence

<220>
<223> universal reverse amplification primer similar to SEQ ID NO:27 and SEQ ID NO:29
<220>
<221> misc_feature
<222> (6)..(6)
<223> inosine

<400> 28
tarttnggrt adatraaytt ytg 23

<210> 29
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> universal reverse amplification primer similar to SEQ ID NO:27 and SEQ ID NO:28
<220>
<221> misc_feature
<222> (18)..(18)
<223> inosine

<400> 29
ggrtadatra aytttgnac 20

<210> 30
<211> 570
<212> DNA

38-21(52806) Sequence Listing_PCT_2.ST25.txt

<213> Bacillus thuringiensis

<220>

<221> CDS

<222> (1)..(570)

<223>

<400> 30

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| ttt | tta | gct | aga | ttt | tgg | ata | ttt | gag | gat | caa | aat | aat | agt | cac | caa | 48 |
| Phe | Leu | Ala | Arg | Phe | Trp | Ile | Phe | Glu | Asp | Gln | Asn | Asn | Ser | His | Gln | |
| 1 | | | | 5 | | | | 10 | | | | | 15 | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| aca | aat | aga | ttt | att | tca | tgg | ttt | aag | gat | aat | att | gct | agt | tca | aaa | 96 |
| Thr | Asn | Arg | Phe | Ile | Ser | Trp | Phe | Lys | Asp | Asn | Ile | Ala | Ser | Ser | Lys | |
| | | | 20 | | | | | 25 | | | | 30 | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ggg | tat | aat | agt | att | gcg | gag | caa | atg | ggg | tta | aaa | ata | gaa | gca | gaa | 144 |
| Gly | Tyr | Asn | Ser | Ile | Ala | Glu | Gln | Met | Gly | Leu | Lys | Ile | Glu | Ala | Glu | |
| | | 35 | | | | 40 | | | | | 45 | | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| aac | gat | atg | gat | gta | aca | aat | ata | gat | tat | aca | tct | aag | aca | ggc | gat | 192 |
| Asn | Asp | Met | Asp | Val | Thr | Asn | Ile | Asp | Tyr | Thr | Ser | Lys | Thr | Gly | Asp | |
| | 50 | | | | | 55 | | | | | 60 | | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| acc | att | tat | aat | ggg | att | tca | gaa | ttg | aaa | aat | tat | aca | gga | tca | act | 240 |
| Thr | Ile | Tyr | Asn | Gly | Ile | Ser | Glu | Leu | Lys | Asn | Tyr | Thr | Gly | Ser | Thr | |
| 65 | | | | 70 | | | | | 75 | | | | | | 80 | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| caa | aag | atg | aaa | aca | gat | agt | ttt | caa | aga | gat | tat | aca | aaa | tca | gaa | 288 |
| Gln | Lys | Met | Lys | Thr | Asp | Ser | Phe | Gln | Arg | Asp | Tyr | Thr | Lys | Ser | Glu | |
| | | | | 85 | | | | 90 | | | | | | 95 | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| tct | act | tca | gta | act | aat | gga | tta | caa | tta | gga | ttt | aaa | gtt | gct | gct | 336 |
| Ser | Thr | Ser | Val | Thr | Asn | Gly | Leu | Gln | Leu | Gly | Phe | Lys | Val | Ala | Ala | |
| | | | 100 | | | | | 105 | | | | | 110 | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| aaa | gga | gta | gtt | gct | ttg | gct | ggg | gca | gac | ttt | gaa | acc | agt | gtt | act | 384 |
| Lys | Gly | Val | Val | Ala | Leu | Ala | Gly | Ala | Asp | Phe | Glu | Thr | Ser | Val | Thr | |
| | | 115 | | | | | 120 | | | | | 125 | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| tat | aat | cta | tca | act | act | aca | act | gaa | aca | aat | aca | ata | tca | gac | aag | 432 |
| Tyr | Asn | Leu | Ser | Thr | Thr | Thr | Thr | Glu | Thr | Asn | Thr | Ile | Ser | Asp | Lys | |
| | 130 | | | | | 135 | | | | | 140 | | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ttt | act | gtc | cca | tct | caa | gaa | gtt | aca | ttg | cct | cca | gga | cat | aaa | gcg | 480 |
| Phe | Thr | Val | Pro | Ser | Gln | Glu | Val | Thr | Leu | Pro | Pro | Gly | His | Lys | Ala | |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ata | gtg | aaa | cat | gat | tta | aga | aaa | atg | gtt | tat | tct | ggg | act | cat | gat | 528 |
| Ile | Val | Lys | His | Asp | Leu | Arg | Lys | Met | Val | Tyr | Ser | Gly | Thr | His | Asp | |
| | | | | 165 | | | | | 170 | | | | | 175 | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|-----|
| cta | aag | ggg | gat | tta | att | gtg | agt | ttt | aat | gat | aaa | gag | att | | | 570 |
| Leu | Lys | Gly | Asp | Leu | Ile | Val | Ser | Phe | Asn | Asp | Lys | Glu | Ile | | | |
| | | | 180 | | | | | 185 | | | | | 190 | | | |

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<210> 31

<211> 190

<212> PRT

<213> Bacillus thuringiensis

<400> 31

Phe Leu Ala Arg Phe Trp Ile Phe Glu Asp Gln Asn Asn Ser His Gln
 1 5 10 15

Thr Asn Arg Phe Ile Ser Trp Phe Lys Asp Asn Ile Ala Ser Ser Lys
 20 25 30

Gly Tyr Asn Ser Ile Ala Glu Gln Met Gly Leu Lys Ile Glu Ala Glu
 35 40 45

Asn Asp Met Asp Val Thr Asn Ile Asp Tyr Thr Ser Lys Thr Gly Asp
 50 55 60

Thr Ile Tyr Asn Gly Ile Ser Glu Leu Lys Asn Tyr Thr Gly Ser Thr
 65 70 75 80

Gln Lys Met Lys Thr Asp Ser Phe Gln Arg Asp Tyr Thr Lys Ser Glu
 85 90 95

Ser Thr Ser Val Thr Asn Gly Leu Gln Leu Gly Phe Lys Val Ala Ala
 100 105 110

Lys Gly Val Val Ala Leu Ala Gly Ala Asp Phe Glu Thr Ser Val Thr
 115 120 125

Tyr Asn Leu Ser Thr Thr Thr Thr Glu Thr Asn Thr Ile Ser Asp Lys
 130 135 140

Phe Thr Val Pro Ser Gln Glu Val Thr Leu Pro Pro Gly His Lys Ala
 145 150 155 160

Ile Val Lys His Asp Leu Arg Lys Met Val Tyr Ser Gly Thr His Asp
 165 170 175

Leu Lys Gly Asp Leu Ile Val Ser Phe Asn Asp Lys Glu Ile
 180 185 190

<210> 32

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<211> 1095

<212> DNA

<213> *Bacillus thuringiensis*

<220>

<221> CDS

<222> (1)..(1092)

<223> sequence encoding TIC431 precursor amino acid sequence

<400> 32

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| atg | aaa | tac | aag | tct | tca | aaa | gta | gca | atg | tgt | aca | tta | tcg | gct | tta | 48 |
| Met | Lys | Tyr | Lys | Ser | Ser | Lys | Val | Ala | Met | Cys | Thr | Leu | Ser | Ala | Leu | |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | | |
| atg | ctt | tcg | aca | atc | gcc | act | cca | agt | ata | tct | ggt | ttc | gct | gct | gaa | 96 |
| Met | Leu | Ser | Thr | Ile | Ala | Thr | Pro | Ser | Ile | Ser | Val | Phe | Ala | Ala | Glu | |
| | | | 20 | | | | | 25 | | | | | 30 | | | |
| aca | act | gca | tca | cat | aag | ggt | act | aat | cag | caa | aca | att | gca | cag | cgt | 144 |
| Thr | Thr | Ala | Ser | His | Lys | Val | Thr | Asn | Gln | Gln | Thr | Ile | Ala | Gln | Arg | |
| | | 35 | | | | 40 | | | | | | 45 | | | | |
| gca | gaa | tct | tat | atc | gat | att | gtg | cat | aat | aga | atg | aaa | aaa | cga | gat | 192 |
| Ala | Glu | Ser | Tyr | Ile | Asp | Ile | Val | His | Asn | Arg | Met | Lys | Lys | Arg | Asp | |
| | 50 | | | | | 55 | | | | | 60 | | | | | |
| att | gaa | tca | aaa | atg | aca | ggg | aaa | cct | att | aat | atg | caa | gaa | caa | ata | 240 |
| Ile | Glu | Ser | Lys | Met | Thr | Gly | Lys | Pro | Ile | Asn | Met | Gln | Glu | Gln | Ile | |
| 65 | | | | | 70 | | | | 75 | | | | | | 80 | |
| att | gat | gga | tgg | ttt | tta | gct | aga | ttt | tgg | ata | ttc | aag | gac | caa | aat | 288 |
| Ile | Asp | Gly | Trp | Phe | Leu | Ala | Arg | Phe | Trp | Ile | Phe | Lys | Asp | Gln | Asn | |
| | | | | 85 | | | | 90 | | | | | | 95 | | |
| aat | agt | cac | caa | aca | aat | aga | ttt | att | tca | tgg | ttt | aaa | gat | aat | tta | 336 |
| Asn | Ser | His | Gln | Thr | Asn | Arg | Phe | Ile | Ser | Trp | Phe | Lys | Asp | Asn | Leu | |
| | | | 100 | | | | | 105 | | | | | 110 | | | |
| gct | agt | cca | gga | ggg | tat | aat | agt | atc | gct | aaa | caa | atg | ggg | tta | aaa | 384 |
| Ala | Ser | Pro | Gly | Gly | Tyr | Asn | Ser | Ile | Ala | Lys | Gln | Met | Gly | Leu | Lys | |
| | | 115 | | | | | 120 | | | | | 125 | | | | |
| ata | gaa | gta | tta | aat | gat | atg | gat | ata | tca | aat | gta | aat | tat | act | tct | 432 |
| Ile | Glu | Val | Leu | Asn | Asp | Met | Asp | Ile | Ser | Asn | Val | Asn | Tyr | Thr | Ser | |
| | 130 | | | | | 135 | | | | | 140 | | | | | |
| aag | aca | ggg | gat | act | ata | tat | aat | ggg | ggt | tcc | gaa | tta | aaa | aat | atc | 480 |
| Lys | Thr | Gly | Asp | Thr | Ile | Tyr | Asn | Gly | Val | Ser | Glu | Leu | Lys | Asn | Ile | |
| 145 | | | | | 150 | | | | 155 | | | | | | 160 | |
| aca | ggg | aca | act | caa | aaa | atg | aaa | aca | gat | agt | ttt | caa | aga | gat | tat | 528 |
| Thr | Gly | Thr | Thr | Gln | Lys | Met | Lys | Thr | Asp | Ser | Phe | Gln | Arg | Asp | Tyr | |
| | | | | 165 | | | | | 170 | | | | | 175 | | |

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| | | | | | | | | | | | | | | | | |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------|
| aca Thr | aaa Lys | tca Ser | cag Gln 180 | tca Ser | act Thr | tca Ser | atc Ile 185 | acc Thr 185 | aat Asn | gga Gly | tta Leu | caa Gln 190 | tta Leu 190 | gga Gly | ttt Phe | 576 |
| aaa Lys | gtt Val | tct Ser 195 | gcc Ala | aaa Lys | ggg Gly | gtg Val 200 | ata Ile 200 | gct Ala | tta Leu | gca Ala | gga Gly 205 | gca Ala 205 | gac Asp | ttc Phe | gaa Glu | 624 |
| gca Ala 210 | agt Ser 210 | gtc Val | aac Asn | tat Tyr | aat Asn 215 | tta Leu 215 | tcc Ser | act Thr | acc Thr | gca Ala | act Thr 220 | gaa Glu | acc Thr | aat Asn | ata Ile | 672 |
| ata Ile 225 | tct Ser | gat Asp | aaa Lys | ttt Phe | acc Thr 230 | gtt Val | cct Pro | tca Ser | caa Gln | gaa Glu 235 | gtt Val | aca Thr | tta Leu | gcg Ala | cca Pro 240 | 720 |
| gga Gly | cat His | aag Lys | gcg Ala 245 | atc Ile 245 | gta Val | aaa Lys | cat His | agt Ser | tta Leu 250 | aag Lys | aaa Lys | atg Met | gta Val | tac Tyr 255 | tcc Ser | 768 |
| gga Gly | acg Thr | cat His | gat Asp 260 | tta Leu | aaa Lys | gga Gly | gat Asp 265 | tta Leu 265 | aca Thr | att Ile | act Thr | ttt Phe | aat Asn 270 | gat Asp | aag Lys | 816 |
| gat Asp | tta Leu | gtt Val 275 | caa Gln | aaa Lys | ttt Phe | att Ile | tat Tyr 280 | cca Pro | aat Asn | tat Tyr | aaa Lys | gct Ala 285 | att Ile | gat Asp | tta Leu | 864 |
| tct Ser 290 | aat Asn 290 | att Ile | cgt Arg | aaa Lys | gca Ala | ctg Leu 295 | act Thr | gaa Glu | att Ile | gat Asp | gaa Glu 300 | tgg Trp | aat Asn | cat His | gta Val | 912 |
| aaa Lys 305 | cct Pro | acc Thr | gat Asp | ttc Phe | tat Tyr 310 | caa Gln | tta Leu | gtt Val | ggg Gly 315 | aac Asn 315 | aaa Lys | aat Asn | tat Tyr | ata Ile | aaa Lys 320 | 960 |
| aac Asn | ggg Gly | gac Asp | act Thr | tta Leu 325 | tac Tyr | atc Ile | gaa Glu | aca Thr | cct Pro 330 | gct Ala | aaa Lys | ttc Phe | act Thr | ttg Leu 335 | aat Asn | 1008 |
| gga Gly | gga Gly | aac Asn | cct Pro 340 | tat Tyr | tat Tyr | aca Thr | gca Ala | acc Thr 345 | ttt Phe | acg Thr | gaa Glu | tat Tyr | gat Asp 350 | gaa Glu | agt Ser | 1056 |
| gga Gly | aat Asn 355 | caa Gln 355 | gtc Val | aaa Lys | aca Thr | aag Lys | cat His 360 | tta Leu | agt Ser | gtc Val | aaa Lys | taa | | | | 1095 |

<210> 33

<211> 364

<212> PRT

<213> Bacillus thuringiensis

<400> 33

Met Lys Tyr Lys Ser Ser Lys Val Ala Met Cys Thr Leu Ser Ala Leu

1 38-21(52806) Sequence Listing_PCT_2.ST25.txt
5 10 15

Met Leu Ser Thr Ile Ala Thr Pro Ser Ile Ser Val Phe Ala Ala Glu
20 25 30

Thr Thr Ala Ser His Lys Val Thr Asn Gln Gln Thr Ile Ala Gln Arg
35 40 45

Ala Glu Ser Tyr Ile Asp Ile Val His Asn Arg Met Lys Lys Arg Asp
50 55 60

Ile Glu Ser Lys Met Thr Gly Lys Pro Ile Asn Met Gln Glu Gln Ile
65 70 75 80

Ile Asp Gly Trp Phe Leu Ala Arg Phe Trp Ile Phe Lys Asp Gln Asn
85 90 95

Asn Ser His Gln Thr Asn Arg Phe Ile Ser Trp Phe Lys Asp Asn Leu
100 105 110

Ala Ser Pro Gly Gly Tyr Asn Ser Ile Ala Lys Gln Met Gly Leu Lys
115 120 125

Ile Glu Val Leu Asn Asp Met Asp Ile Ser Asn Val Asn Tyr Thr Ser
130 135 140

Lys Thr Gly Asp Thr Ile Tyr Asn Gly Val Ser Glu Leu Lys Asn Ile
145 150 155 160

Thr Gly Thr Thr Gln Lys Met Lys Thr Asp Ser Phe Gln Arg Asp Tyr
165 170 175

Thr Lys Ser Gln Ser Thr Ser Ile Thr Asn Gly Leu Gln Leu Gly Phe
180 185 190

Lys Val Ser Ala Lys Gly Val Ile Ala Leu Ala Gly Ala Asp Phe Glu
195 200 205

Ala Ser Val Asn Tyr Asn Leu Ser Thr Thr Ala Thr Glu Thr Asn Ile
210 215 220

Ile Ser Asp Lys Phe Thr Val Pro Ser Gln Glu Val Thr Leu Ala Pro
225 230 235 240

Gly His Lys Ala Ile Val Lys His Ser Leu Lys Lys Met Val Tyr Ser
245 250 255

38-21(52806) Sequence Listing_PCT_2.ST25.txt

Gly Thr His Asp Leu Lys Gly Asp Leu Thr Ile Thr Phe Asn Asp Lys
260 265 270

Asp Leu Val Gln Lys Phe Ile Tyr Pro Asn Tyr Lys Ala Ile Asp Leu
275 280 285

Ser Asn Ile Arg Lys Ala Leu Thr Glu Ile Asp Glu Trp Asn His Val
290 295 300

Lys Pro Thr Asp Phe Tyr Gln Leu Val Gly Asn Lys Asn Tyr Ile Lys
305 310 315 320

Asn Gly Asp Thr Leu Tyr Ile Glu Thr Pro Ala Lys Phe Thr Leu Asn
325 330 335

Gly Gly Asn Pro Tyr Tyr Thr Ala Thr Phe Thr Glu Tyr Asp Glu Ser
340 345 350

Gly Asn Gln Val Lys Thr Lys His Leu Ser Val Lys
355 360